

**REMARKS**

The Communication required submission of a computer readable and paper copy of the sequence listing.

It is respectfully asserted that the sequence disclosure contained in the application now fully complies with the requirements set forth in 37 C.F.R. § 1.821 to § 1.825.

It is respectfully submitted that the Sequence Listing conforms to the requirements of 37 C.F.R. §1.823(b). The Statements required by 37 C.F.R §1.821(f) and (g) are set forth below.

Pursuant to 37 C.F.R. §1.821 (g), the undersigned hereby states that this submission, filed in accordance with 37 C.F.R. §1.821 (g), does not contain new matter.


Pursuant to 37 C.F.R. §1.821 (f), the undersigned hereby states that the content of the paper and computer readable copies of the Sequence Listing submitted in accordance with 37 C.F.R. §1.821 (c) and (e), respectively, are the same.

CONCLUSION

In view of the amendments, remarks and enclosures herein, it is respectfully submitted that the application now complies with all requirements set forth in the Communication, including the requirements for computer readable disclosure of the biological sequences under 37 C.F.R. §1.821-1.825. Reconsideration and withdrawal of the objections are earnestly solicited.

Respectfully submitted,

FROMMER LAWRENCE & HAUG LLP  
Attorneys for the Applicant

By:   
William S. Frommer  
Reg. No. 25,506  
(212) 588-0800

Enclosures: -Paper copy of Sequence Listing  
-Computer Readable Copy of Sequence Listing  
-Copy of the Communication



## UNITED STATES PATENT AND TRADEMARK OFFICE



UNITED STATES DEPARTMENT OF COMMERCE  
United States Patent and Trademark Office  
Address: COMMISSIONER OF PATENTS AND TRADEMARKS  
Washington, D.C. 20231  
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/677,672	10/02/2000	Jean-Christophe Francis Audonnet	454313-3160	3424

20999 7590 06/06/2002

FROMMER LAWRENCE & HAUG  
745 FIFTH AVENUE- 10TH FL.  
NEW YORK, NY 10151

EXAMINER

NGUYEN, DAVE TRONG

ART UNIT PAPER NUMBER

1632

DATE MAILED: 06/06/2002

*deleted: July 6, 2002*  
*Sequence Listing*

Please find below and/or attached an Office communication concerning this application or proceeding.

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Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
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09/677,672

10/02/2000

Audonnet

EXAMINER
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DAVE NGUYEN

ART UNIT	PAPER NUMBER
----------	--------------

1632

6

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application.

Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications regarding the formalities should be directed to Patent Analyst Dianiece Jacobs, whose telephone number is (703) 305-3388.

Any inquiry concerning this communication or earlier communications from the

examiner should be directed to examiner *Dave Nguyen* whose telephone number is **(703) 305-2024**.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, *Deborah Reynolds*, may be reached at **(703) 305-4051**.

Papers related to this application may be submitted to Group 1600 by facsimile transmission. Papers should be faxed to Group 1600 via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). The CM1 Fax Center number is **(703) 305-7401**.

Any inquiry of a general nature or relating to the status of this application should be directed to the *Group receptionist* whose telephone number is **(703) 308-0196**.

Dave Nguyen  
Primary Examiner  
Art Unit: 1632

  
DAVE T. NGUYEN  
PRIMARY EXAMINER



Application No.: 09/677,672

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: Please see the attached Raw Sequence Listing Error Summary

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

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1095  
D

**RAW SEQUENCE LISTING  
ERROR REPORT**

Re-run

BIOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/677,672

Source: O/PK

Date Processed by STIC: 10/13/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Ra Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/672,672

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE



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- 1      **Wrapped Nucleics**      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      **Wrapped Aminos**      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3      **Incorrect Line Length**      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      **Misaligned Amino Acid Numbering**      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      **Non-ASCII**      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      **Variable Length**      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7      **PatentIn ver. 2.0 "bug"**      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8      **Skipped Sequences (OLD RULES)**      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      **Skipped Sequences (NEW RULES)**      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10      **Use of n's or Xaa's (NEW RULES)**      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      **Use of <213>Organism (NEW RULES)**      Sequence(s)      are missing this mandatory field or its response.
- 12      **Use of <220>Feature (NEW RULES)**      Sequence(s)      are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      **PatentIn ver. 2.0 "bug"**      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.





RAW SEQUENCE LISTING

DATE: 10/13/2000

PATENT APPLICATION: US709/677,672

TIME: 08:27:22

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Output Set: N:\CRF3\10132000\I677672.raw

3 <110> APPLICANT: AUDONNET et al.  
 5 <120> TITLE OF INVENTION: ADJUVANT CONTAINING DNA VACCINES  
 7 <130> FILE REFERENCE: 454313-3160  
 9 <140> CURRENT APPLICATION NUMBER: US/09/677,672  
 10 <141> CURRENT FILING DATE: 2000-10-02  
 12 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00666  
 13 <151> PRIOR FILING DATE: 1999-03-22  
 15 <150> PRIOR APPLICATION NUMBER: 98 04409 FRANCE  
 16 <151> PRIOR FILING DATE: 1998-04-03  
 18 <160> NUMBER OF SEQ ID NOS: 13  
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 23 <211> LENGTH: 40  
 24 <212> TYPE: DNA  
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 26 <400> SEQUENCE: 1 *valid responses for <213> are: Unknown or*  
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 31 <211> LENGTH: 34  
 32 <212> TYPE: DNA  
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 45 gtaaaaaaaa taactgatga ccaaatgtag gtgacaaatg ctactgaatt agtccagagc 180  
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 48 ctcttcatag aaagaagcag cgctttcagc aattgctacc catatgacat ccctgactat 360  
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 61 atggttgatg ggtggtatgg attccgatat caaaactcgg aaggaacagg acaagctgca 1140

Does Not Comply  
Corrected Diskette Needed

pp. 1-5

(global env)

The only

valid responses for <213> are: Unknown or

Artificial Sequence

or scientific name

(Genus/species)

See 1.823 of

new sequence

Rules. See, also

circled portion

of item 12 on

Errata Summary

sheet.

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/677,672

DATE: 10/13/2000  
TIME: 08:27:23

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114 ttaatttgcg ttgttctatt gggtttcatt atgtgggctt gccaaaaagg caacatcaga 1680
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/677,672

DATE: 10/13/2000

TIME: 08:27:22

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Output Set: N:\CRF3\10132000\I677672.raw



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159 gatatacggt ttctttcaca ttgccggttg aactaacaaa aaagggatgt ttagtccct 1260
160 gtttctgggt tgaaatgatt agaggtaaac ctgaagaaac aacaatatg acctctagca 1320
161 gctccattgt gatgtgfgga gtagatcata aagttgccag ttggtcatg cagatggag 1380
162 ctattcttcc ctttgacatc gataagatgt aa
165 <210> SEQ ID NO: 9
166 <211> LENGTH: 1414
167 <212> TYPE: DNA
W--> 169 <213> ORGANISM:
169 <400> SEQUENCE: 9
170 atgaatccaa atcaaaagat aataacaatt ggaatcgcat cattgggaat ataatcacc 60
171 aacgtcattc tccatgtagt cagcattata gtaacagtac tggctctcaa taacaatgga 120

```

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## RAW SEQUENCE LISTING

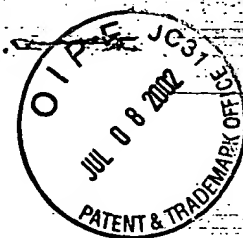
DATE: 10/13/2000

PATENT APPLICATION: US/09/677,672

TIME: 08:27:22

Input Set : A:\Audonnel.app

Output Set: N:\CRF3\10132000\I677672.raw



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172 acaggctctga actgcaagg gacgatcata agagagtaca atgaaccaat aagagtagaa 180
173 agaattactc aatggtataa taccagtaca attgagtaca tagagagacc tcaaatgaa 240
174 tactacatga acaacaccga accactttgt gaggcccaag gctttgcacc attttccaaa 300
175 gataatggaa tacgaattgg gtcgagaggg catgtttttg taataaggaga acctttttgc 360
176 tcatgtttgc cctcagaatg tagaaccttt ttctcacac aggggttcatttactcaatgac 420
177 aaacattcta acggcacagt gaaggaccga agtccatata ggactttgat gagggtcaaa 480
178 atagggcaat cacttaagt gtatcaagct aggtttgaat cgggtggcatg gtcagcaaca 540
179 gcatgccatg atgaaaaaaa atggatgaca gttggagtca caggggccga taatcaagca 600
180 attgcagttag tgaactatgg aggtgttccg gttgatatta ttaattcatg ggcaggggat 660
181 atcttaagaa cccaagaatc gtcatgcacc tgcattaaag gagactgtta ttgggtgatg 720
182 attgatggac cggcaaatag gcaagctaaa tataggatat tcaaaagcaa agatggaaga 780
183 aattgggc agactgatat aagtttcaat gggggacaca tagaggagtg ttcttggttac 840
184 cccaatgaag ggaaggtgga atgcataatc agggacaact ggactggaac aaatagacca 900
185 attctggtta tatcttctga tctatcgtac acagtcggat atttgtgtgc tggcattccc 960
186 actgacactc ctaggggaga ggatagtcaa ttcacaggct catgtacaag tcctttggga 1020
187 aataaaggat acggtgtaaa aggtttcggg ttccgacaag gaactgacgt atgggcccga 1080
188 aggacaatta gtaggacttc aagatcagga ttcgaaataa taaaaatcag gaatggttgg 1140
189 acacagaaca gtaaaagcca aatcagaagg caagtgtatta ttgatacccc aaattggtca 1200
190 ggatatagcg gttctttcac attgcccgtt gaactaacia aaaagggata gtttagtccc 1260
191 ctgtttctgg gttgaaatga tttagaggtaa acctgaagaa acaacaatat ggacctctag 1320
192 cagctccatt gtgatgtgtg gagtagatca taaaattgcc agttgtgcat ggcacgatgg 1380
193 agctattctt ccttttgaca tagacaagat gtatg 1414
196 <210> SEQ ID NO: 10
197 <211> LENGTH: 26
198 <212> TYPE: DNA
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200 <400> SEQUENCE: 10
201 ttgtcgacca tggcgtctca aggcac 26
204 <210> SEQ ID NO: 11
205 <211> LENGTH: 28
206 <212> TYPE: DNA
W--> 208 <213> ORGANISM:
208 <400> SEQUENCE: 11
209 ttcttagact ttaaytgta wactcytc 28
212 <210> SEQ ID NO: 12
213 <211> LENGTH: 1497
214 <212> TYPE: DNA
W--> 216 <213> ORGANISM:
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218 aatgcaactg aaatcagagc atctgtcggg aggatgggtg gaggaaatcg ccggttttat 120
219 gttcagatgt gtactgagct taaattaaac gacctgaag ggcggtgat tcagaacagc 180
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221 gagcatccca gtgctgggaa agaccctaag aaaacgggag gccgatata cagaaggaaa 300
222 gatgggaaat ggataagaga actcatcctc catgataaag aggaaatcat gagggctctg 360
223 cgtcaggcca acaatggtga agatgctact gctgtctta cccatgatg gatctggcac 420
224 tccaatctca atgacaccac ataccaaaaga acaagggctc ttgttcggac tgggatggat 480
225 cccagaatgt gctctctgat gcaaggatca accctccac ggagatctgg agctgccggt 540
226 gctgcagtaa aaggtgttgg aacaatgata atggaactca tcaggatgat caaacgcggg 600

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/677,672

DATE: 10/13/2000

TIME: 08:27:22

Input Set : A:\Audonnel.app

Output Set: W:\CRF3\10132000\I677672.raw

227-ataaatgac gaaatttctg gagaggtgaa aatggctgaa gaaccagaat tgcctatgaa 660  
 228-agaatgtgca atatcctcaa agggaaattt caaacagcag cacaacgggc tatgatggaa 720  
 229-ccaagtggg gaggggccgca atcctggaaa tgctgagatt gaggatctca tttcttggc 780  
 230-acgatcagca ctcatttggg aggatcagta gcccataaat catgacctacc tgcctgtgt 840  
 231-tatggccttg cagtaaccag tgggtatgac ttgagaagg aaggatactc tctgttggg 900  
 232-attgatcctt tcaaaactct ccagaacagc caaattttca gctaatcag accgaagaa 960  
 233-aatccagcac acaagagcca gttggtgtg atggcatgcc attctgcagc atttgaggac 1020  
 234-ctgagagtgt tgaatttcat tagaggaaca aaagtaatcc caaggagaca gttggcaacc 1080  
 235-agaggagtgc agattgtctc aaatgaaaac atggagaaca atagattcta gcacactcga 1140  
 236-actgagaagc agatattggg caataaggac cagaagtggg gaaacacca gtcaacagag 1200  
 237-gcatctgca ggacagataa gtgtgcaacc tacttttcca gtgcagagaa atcttccctt 1260  
 238-gaaagagca accattatgg ctgcatttac tgggaacact gagcggagga cttccgacat 1320  
 239-gagaacggaa atcataagga tgatggaaaa tgccaaatca gaagatgtgt ctttccaggg 1380  
 240-gcggggagtc ttcgagctct cggacgaaaa ggcaacgaac ccgatcgtgc cttcctttga 1440  
 241-catgacaatg aagggtctta tttcttcgga gacaatgctg agggagtatga cagttaa 1497

244 &lt;210&gt; SEQ ID NO: 13

245 &lt;211&gt; LENGTH: 1493

246 &lt;212&gt; TYPE: DNA

W--&gt; 248 &lt;213&gt; ORGANISM:

248 &lt;400&gt; SEQUENCE: 13

249 atggcgtctc aaggcaccac acgatcttat gagcagatgg aaactgatgg ggaacgccag 60  
 250 aatgcaactg aaatcagagc atctgtcggg aggatgggtg gaggaatcgg ccggttttat 120  
 251 gttccagatg tgtactgagc ttaaaactaaa cgaccatgaa gggcggctga ttcagaacag 180  
 252 cataacaata gaaaggtatg tactctcggc attcgcagaa agaagaaaca agtatctcga 240  
 253 ggagcatccc agtctgggga aagaccctaa gaaaacggga ggcccgatat acagaaggaa 300  
 254 agatgggaaa tggatgagag aactcatcct ccattgataa gaagaaatca tgaggatctg 360  
 255 gcgtcaggcc aacaatgtgt aagacgctac tgctgtgtctt actcatatga tgatctggca 420  
 256 ctccaatctc aatgacacca aagaacaagg gctcttgttc ggactgggat ggaatccaga 480  
 257 atgtgtcttc tgatgcaagg ctcaaccctc ccacggagat ctggagccgc tgggtgtgca 540  
 258 gtaaaagggt ttggaacaat ggtaatggaa ctcatcagaa tgatcaaacg cgggataaat 600  
 259 gatcggaatt tctggagagg tgaatatagg tcgaagaacc agaattgctt atgaaagaat 660  
 260 gtgcaatcct ctcaagggga aatttcagac agcagcacaa cgggctatga tggaccaggt 720  
 261 gagggaaagg cgcaatctct gaaacgctga gattgaggat ctcatcttct tggcacgac 780  
 262 agcacttatt ttgagaggat cagtagccca taaatcatgc ctacctgcct gtgtttatgg 840  
 263 ccttgcaaga accagtgggt atgactttga gaaggaagga tactctctgg ttggaattga 900  
 264 tcttttcaaa ctactccaga acagcccaat tttcagtcta atcagaccga aagaaaaccc 960  
 265 agcacacaag agccagttgg tgtggatggc atgccattct gcagcatttg aggacctgag 1020  
 266 agttttgaat ttcatatgag gaaccaaagt aatcccaaga ggacagttag caaccagagg 1080  
 267 agtgcaaatg gcttcaaatg aaaacatgga gacaatagat tctagcacac tcgaactgag 1140  
 268 aagcaaatat tgggcaataa ggaccagaag tggaggaaaa caccagtcaa cagagagcat 1200  
 269 ctgcaggaca gataagtgtg caacctactt tctcagtgtc gagaaatctt ccttttga 1260  
 270 gagcaacctat tatggctgtc ttcactggga aactgaagg gaggacttcc gacatgagaa 1320  
 271 cggaaatcat aaggatgatg gaaaatgcca aatcagaaga tgtgtcttcc caggggcggg 1380  
 272 gagtcttcga gctctcggac gaaaaggcaa cgaaccgat cgtgccttcc tttgacatga 1440  
 273 gcaatgaagg gtcttatttc ttcggagaca atgctgagga gtttgacaat taa 1493



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## VERIFICATION SUMMARY

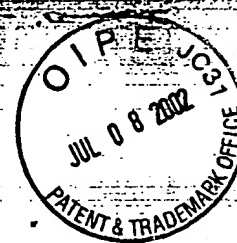
PATENT APPLICATION: US/09/677,672

DATE: 10/13/2000

TIME: 08:27:23

Input Set : A:\Audonnel.app

Output Set : N:\CRF3\10132000\I677672.raw



L:9 M:270 C: Current Application Number differs, Replaced Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:26 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:34 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:42 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:78 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:86 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:122 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:130 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:138 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:169 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:200 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:208 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:216 M:282 W: Numeric Field Identifier Missing, <213> is required  
L:248 M:282 W: Numeric Field Identifier Missing, <213> is required

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